#### RAW SEQUENCE LISTING PATENT APPLICATION US/08/443,982A

DATE: 04/17/96 TIME: 14:47:34

36

INPUT SET: S9946.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

1		SEQUENCE LISTING	•
2 3	(1) G	SEQUENCE LISTING PROPERTY OF THE PROPERTY OF T	J
4	(1) G	eneral iniormation.	
5 6 7	(i)	APPLICANT: DIXIT, VISHVA M. O'ROURKE, KAREN	
8 9	(ii)	TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING FAS-ASSOCIATED APOPTOSIS	3
10 11 12	(iii)	NUMBER OF SEQUENCES: 10	
13 14 15 16 17 18 19	(iv)	CORRESPONDENCE ADDRESS:  (A) ADDRESSEE: Morrison & Foerster  (B) STREET: 755 Page Mill Road  (C) CITY: Palo Alto  (D) STATE: CA  (E) COUNTRY: USA  (F) ZIP: 94304-1018	
21 22 23 24 25 26	(v)	COMPUTER READABLE FORM:  (A) MEDIUM TYPE: Floppy disk  (B) COMPUTER: IBM PC compatible  (C) OPERATING SYSTEM: PC-DOS/MS-DOS  (D) SOFTWARE: PatentIn Release #1.0, Version #1.30	
27 28 29 30 31	(vi)	CURRENT APPLICATION DATA:  (A) APPLICATION NUMBER: US 08/443,982  (B) FILING DATE: 18-MAY-1995  (C) CLASSIFICATION:	
32 33 34 35 36	(Viii)	ATTORNEY/AGENT INFORMATION:  (A) NAME: Konski, Antoinette F.  (B) REGISTRATION NUMBER: 34,202  (C) REFERENCE/DOCKET NUMBER: 20344-21070.20	
37 38 39 40 41	(ix)	TELECOMMUNICATION INFORMATION: (A) TELEPHONE: (415)813-5600 (B) TELEFAX: (415)494-0792 (C) TELEX: 706141 MRSNFOERS SFO	
42	(2) INFO	RMATION FOR SEQ ID NO:1:	
44 45	(4)	CECHENGE GUADACHEDICHICO.	
45	(1)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 1642 base pairs	
- <del>-</del> 2 U		(v) neggin, igas pase bails	

#### RAW SEQUENCE LISTING PATENT APPLICATION US/08/443,982A

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INPUT SET: S9946.raw
47
               (B) TYPE: nucleic acid
48
               (C) STRANDEDNESS: single
               (D) TOPOLOGY: linear
49
50
         (ii) MOLECULE TYPE: cDNA
51
52
53
54
         (ix) FEATURE:
               (A) NAME/KEY: CDS
55
56
               (B) LOCATION: 130..756
57
         (ix) FEATURE:
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59
               (A) NAME/KEY: misc feature
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               (B) LOCATION: 4..6
61
               (D) OTHER INFORMATION: /note= "An in-frame stop codon 130
62
      base pairs upstream of the initiator methionine"
63
         (ix) FEATURE:
64
65
               (A) NAME/KEY: polyA signal
66
               (B) LOCATION: 1636..1641
67
               (D) OTHER INFORMATION: /note= "Potential poly(A)
68
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69
         (ix) FEATURE:
70
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72
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75
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               (D) OTHER INFORMATION: /note= "Death Domain of FADD"
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85
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86
               (A) NAME/KEY: mutation
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               (D) OTHER INFORMATION: /note= "For FADDmt: sequence is altered to either
88
89
      the codon from Val to Asn"
90
91
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94
               (D) OTHER INFORMATION: /note= "Codons can comprise
95
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96
97
         (ix) FEATURE:
98
               (A) NAME/KEY: misc feature
99
               (B) LOCATION: 253..753
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## RAW SEQUENCE LISTING PATENT APPLICATION US/08/443,982A

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100	(D) OTHER INFORMATION: /note= "Codons can comprise polypeptide fragment of FADD designated NFD-2"													
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106	(D) OTHER INFORMATION: /note= "Codons can comprise													
107	polypeptide fragment of FADD designated NFD-3"													
108														
109	(ix) FEATURE:													
110	(A) NAME/KEY: misc_feature													
111	(B) LOCATION: 367753													
112	(D) OTHER INFORMATION: /note= "Codons can comprise													
113	polypeptide fragment of FADD designated NFD-4"													
114														
115	(ix) FEATURE:													
116	(A) NAME/KEY: misc_feature													
117														
118														
119														
120														
121	(ix) FEATURE:													
122	(A) NAME/KEY: misc feature													
123	(B) LOCATION: 133501													
124	Y Y													
125	•													
126														
127														
127 128	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:													
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:													
128	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG	60												
128 129		60												
128 129 130		60 120												
128 129 130 131	CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG													
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128 129 130 131 132 133 134 135	CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CAC TCG GTG TCC Met Asp Pro Phe Leu Val Leu His Ser Val Ser Ser	120												
128 129 130 131 132 133 134 135	CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CAC TCG GTG TCC Met Asp Pro Phe Leu Val Leu His Ser Val Ser Ser  1 5 10	120												
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128 129 130 131 132 133 134 135 136 137	CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CAC TCG GTG TCC Met Asp Pro Phe Leu Val Leu His Ser Val Ser Ser 1 5 10  AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG	120 168												
128 129 130 131 132 133 134 135 136 137 138	CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CAC TCG GTG TCG TCC Met Asp Pro Phe Leu Val Leu His Ser Val Ser Ser 1 5 10  AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG Ser Leu Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly	120 168												
128 129 130 131 132 133 134 135 136 137 138	CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CAC TCG GTG TCG TCC Met Asp Pro Phe Leu Val Leu His Ser Val Ser Ser 1 5 10  AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG Ser Leu Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly	120 168												
128 129 130 131 132 133 134 135 136 137 138 139 140	CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CAC TCG GTG TCG TCC Met Asp Pro Phe Leu Val Leu His Ser Val Ser Ser 1 5 10  AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG Ser Leu Ser Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly 15 20 25  CGC GTG GGC AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC	120 168 216												
128 129 130 131 132 133 134 135 136 137 138 139 140 141	CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CAC TCG GTG TCC Met Asp Pro Phe Leu Val Leu His Ser Val Ser Ser  1 5 10  AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG Ser Leu Ser Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly  15 20 25	120 168 216												
128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143	CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CAC TCG GTG TCG TCC Met Asp Pro Phe Leu Val Leu His Ser Val Ser Ser 1 5 10  AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG Ser Leu Ser Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly 15 20 25  CGC GTG GGC AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu	120 168 216												
128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144	CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CAC TCG GTG TCG TCC Met Asp Pro Phe Leu Val Leu His Ser Val Ser Ser 1 5 10  AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG Ser Leu Ser Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly 15 20 25  CGC GTG GGC AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu	120 168 216												
128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144	CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG  GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA  GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CAC TCG GTG TCC Met Asp Pro Phe Leu Val Leu His Ser Val Ser Ser 1 5 10  AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG Ser Leu Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly 15 20 25  CGC GTG GGC AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu 30 35 40 45  TTC TCC ATG CTG CTG GAG CAG AAC GAC CTG GAG CCC GGG CAC ACC GAG	120 168 216												
128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144	CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CTG CAC TCG GTG TCC Met Asp Pro Phe Leu Val Leu His Ser Val Ser Ser 1 5 10  AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG Ser Leu Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly 15 20 25  CGC GTG GGC AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu 30 35 40 45	120 168 216												
128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147	CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG  GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCCGGCCCGGCCCTTGCA  GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CTG CAC TCG GTG TCC Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser 1 5 10  AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG Ser Leu Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly 15 20 25  CGC GTG GGC AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu 30 35 40 45  TTC TCC ATG CTG CTG GAG CAG AAC GAC CTG GAG CCC GGG CAC ACC GAG Phe Ser Met Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu	120 168 216												
128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148	CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG  GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA  GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CTC CAC TCG GTG TCG TCC  Met Asp Pro Phe Leu Val Leu His Ser Val Ser Ser  1 5 10  AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG Ser Leu Ser Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly  15 20 25  CGC GTG GGC AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu  30 35 40 45  TTC TCC ATG CTG CTG GAG CAG AAC GAC CTG GAG CCC GGG CAC ACC GAG Phe Ser Met Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu  50 55 60	120 168 216												
128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150	CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG  GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA  GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CAC TCG GTG TCG TCC  Met Asp Pro Phe Leu Val Leu His Ser Val Ser Ser  1 5 10  AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG Ser Leu Ser Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly  15 20 25  CGC GTG GGC AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu  30 35 40 45  TTC TCC ATG CTG CTG GAG CAG AAC GAC CTG GAG CCC GGG CAC ACC GAG Phe Ser Met Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu  50 55 60  CTC CTG CGC GAG CTG CTC CTC CTG CGG CGC CAC GAC CTG CGG	120 168 216 264												
128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148	CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG  GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA  GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CTC CAC TCG GTG TCG TCC  Met Asp Pro Phe Leu Val Leu His Ser Val Ser Ser  1 5 10  AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG Ser Leu Ser Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly  15 20 25  CGC GTG GGC AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu  30 35 40 45  TTC TCC ATG CTG CTG GAG CAG AAC GAC CTG GAG CCC GGG CAC ACC GAG Phe Ser Met Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu  50 55 60	120 168 216 264												

## RAW SEQUENCE LISTING PATENT APPLICATION US/08/443,982A

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153 154	aaa	CTIC	CAC	GAC	TITE C	a v a	aaa	aaa	aaa	aaa	aaa	aaa	000	aaa	COM	aaa	. 400
																	408
155	Arg	νац		Asp	Pne	GIU	Ата		ATA	АТА	АТа	GTA		Ата	PIO	GIÀ	
156			80					85					90				
157	~	~	010	ama	mam	991	<b>aa</b> .			ama		mam	~~~		ama.	000	
158				CTG													456
159	GIU		Asp	Leu	cys	АТа		Pne	Asn	Val	IIe	_	Asp	Asn	vaı	GTÀ	
160		95					100					105					
161																	
162				AGA													504
163		Asp	Trp	Arg	Arg		Ala	Arg	Gln	Leu	_	Val	Ser	Asp	Thr	-	
164	110					115					120					125	
165																	
166				ATC													552
167	Ile	Asp	Ser	Ile	Glu	Asp	Arg	Tyr	Pro	Arg	Asn	Leu	Thr	Glu	Arg	Val	
168					130					135					140		
169																	
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171	Arg	Glu	Ser	Leu	Arg	Ile	Trp	Lys	Asn	Thr	Glu	Lys	Glu	Asn	Ala	Thr	
172				145					150					155			
173																	
174	GTG	GCC	CAC	CTG	GTG	GGG	GCT	CTC	AGG	TCC	TGC	CAG	ATG	AAC	CTG	GTG	648
175	Val	Ala	His	Leu	Val	Gly	Ala	Leu	Arg	Ser	Cys	Gln	Met	Asn	Leu	Val	
176			160					165					170				
177				•													
178	GCT	GAC	CTG	GTA	CAA	GAG	GTT	CAG	CAG	GCC	CGT	GAC	CTC	CAG	AAC	AGG	696
179	Ala	Asp	Leu	Val	Gln	Glu	Val	Gln	Gln	Ala	Arg	Asp	Leu	Gln	Asn	Arg	
180		175					180				_	185				-	
181																	
182	AGT	GGG	GCC	ATG	TCC	CCG	ATG	TCA	TGG	AAC	TCA	GAC	GCA	TCT	ACC	TCC	744
183				Met													
184	190	_				195			_		200	-				205	
185																	
186	GAA	GCG	TCC	TGA	TGG	CCGC	CTG (	TTTC	3CGC1	rg gr	rggac	CAC	A GG	CATC	<b>FACA</b>		796
187		Ala															
188																	
189																	
190	CAG	CCTG	GAC '	TTTG	GTTC:	C TO	CAG	BAAGO	TAC	3CCC#	AGCA	CTGT	GAAC	GAC (	CCAG	CAGGAA	856
191																	
192	GCC	AGGC'	rga (	GTGA	CCAC	CA GA	ACCAC	CTGC	TTC	TGA	ACTC	AAGO	CTGC	TT :	TATTA	ATGCC	916
193																	
194	TCT	CCCG	CAC	CAGG	CCGG	C T	rggg	CCTC	CAC	CAGAT	TTAT	TCC	ATTTC	CTT (	CCTC	CTATG	976
195																	
196	ACAG	CTGA	GCA .	AGAT	CTTGT	C TO	CACT	'AAA'	GAC	CTC	CTGC	GGG	GTAG	TT (	GAAZ	AGTTGG	1036
197																	
198	AAC	CGTG	rcc .	AGCA	CAGA	AG GA	ATCI	GTGC	AGA	ATGAC	CAG	TCAC	CACTO	TT I	ACTC	CACAGC	1096
199																	
200	GGAG	GAG	ACC	AGCT	CAGAC	ag co	CAGO	TAATO	GGZ	AGCG	AAGC	AGAC	AGG	rgg i	AGAAC	CTGGGA	1156
201		•	<b>-</b> .														
202	ТТТС	BAAC	ccc (	CGCC2	ATCCT	т с	ACCAC	BAGCC	CAT	rgctro	CAAC	CACT	יפייפי	agg r	יייריייי	CTGCC	1216
203	`			1													
204	ССТО	GCAG	rtg (	GCAG	AAAG	A TO	3TTTT	CTCC	CAT	TTCC	TTG	GAGO	CCAC	CCG (	GAC	GACCT	1276
205																	

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## RAW SEQUENCE LISTING PATENT APPLICATION US/08/443,982A

DATE: 04/17/96 TIME: 14:47:48

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206 207	GGA	CACTA	AGG (	STCA	36060	3G G	rgere	GTGG	r GG	GGAG	AGGC	ATG	3CTG	GGG	TGGGG	GGTGGG	1336
208 209	GAG	ACCTO	GGT :	rggc	CGTG	T C	CAGC'	rctt(	G GC	CCCT	GTGT	GAG'	rtga(	GTC	TCCT	CTCTGA	1396
210 211	GAC	rgcti	AAG	ragg	GCA	GT G	ATGG'	TTGC	C AG	GACG	AATT	GAG	ATAA'	TAT	CTGT	GAGGTG	1456
212 213	CTG	ATGA	GTG A	ATTG	ACAC	AC A	GCAC'	rctc:	Г АА	ATCT'	rcct	TGT	GAGG	ATT	ATGG	STCCTG	1516
214 215	CAAT	rtcti	ACA (	3TTT(	CTTAC	CT G'	TTTT	GTAT	CAA	AATC	ACTA	TCT	rtct(	GAT	AACA	GAATTG	1576
216 217	CCA	AGGC	AGC (	GGGA!	CTC	GT A'	TCTT'	ГААА	A· AG	CAGT	CCTC	TTA	rtcc'	TAA	GGTA	ATCCTA	1636
218 219	TTA	AAA															1642
220																	
221 222	(2)	INF	ORMA'	rion	FOR	SEQ	ID 1	NO:2	:								
223			(i) S	SEQUI	ENCE	CHA	RACTI	ERIS	rics	:							
224				( A	) LEI	NGTH	: 20	08 ar	nino	acio	<b>l</b> s						
225				(B	TYF)	PE: 8	amin	o ac	id								
226				( D	TOI	POLO	GY:	linea	ar								
227																	
228		( )	ii) 1	MOLE	CULE	TYP	E: p	rote:	in								
229																	
230		( 2	Ki) S	SEQUI	ENCE	DES	CRIP	rion:	: SE	O ID	NO:2	2:					
231		_	_		_		_	_		_		_		_	_	_	
232		Asp	Pro	Phe		Val	Leu	Leu	Hıs		Val	Ser	Ser	Ser	Leu	Ser	
233	1				5					10					15		
234		C	a1	T	mb	<b>a</b> 1	T	T	Dh a	T	<b>a</b>	T	<b>~</b> 1	<b>3</b>	**- 7	a1	
235 236	ser	ser	GIU	20	Thr	GLU	Leu	ьys	25	Leu	cys	ren	GTA	_	Val	GTA	
236				20					25					30			
237	Tue	۸ra	Tue	T 011	Glu.	λrα	Val	Cln.	Sor	al v	T OIL	λen	Γ 011	Pho	Ser	Mot	
239	цуз	Arg	35	Leu	Giu	Arg	Val	40	Ser	сту	пеп	АЗР	45	File	Ser	мес	
240													43				
241	Leu	Leu	Glu	Gln	Asn	Asp	Leu	Glu	Pro	Glv	His	Thr	Glu	Leu	Leu	Ara	
242		50	. —				55			2		60				5	
243																	
244	Glu	Leu	Leu	Ala	Ser	Leu	Arg	Arg	His	Asp	Leu	Leu	Arg	Arg	Val	Asp	
245	65					70	_	_		_	75		_	_		80	
246																	
247	Asp	Phe	Glu	Ala	Gly	Ala	Ala	Ala	Gly	Ala	Ala	Pro	Gly	·Glu	Glu	Asp	
248					85					90					95		
249																	
250	Leu	Cys	Ala		Phe	Asn	Val	Ile		Asp	Asn	Val	Gly	Lys	Asp	Trp	
251				100					105					110			
252		_	_		_		_				_ 0		_		_	_	
253	Arg	Arg		Ala	Arg	Gln	Leu		Val	Ser	Asp	Thr	_	Ile	Asp	Ser	
254			115					120					125				
255	T7.	03	N	A	m	D=-	N	N	T	ml	<b>41.</b>	<b>3</b>	17. 7	3	α1	<b>0</b>	
256 257	тте		ASP	arg	TAL	PIO	_	ASN	ьец	rnr	GTU	-	vaı	arg	Glu	ser	
257 258		130					135					140					

# **SEQUENCE VERIFICATION REPORT** PATENT APPLICATION *US/08/443,982A*

DATE: 04/17/96 TIME: 14:47:51

INPUT SET: S9946.raw

Line

Error

Original Text

271

Stop Codon at end of sequence removed - no error